

GEPHE SUMMARY

Zmr1 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> )	Gephebase Gene	GP00001715	GepheID
Gephebase= <sup>^</sup> Zmr1 <sup>^</sup> #gephebase-summary-title)			Main curator
Published	Entry Status	Courtier	

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> )	Category= <sup>^</sup> Physiology <sup>^</sup> #gephebase-summary-title)
Xenobiotic resistance (fungicide) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=&lt;sup&gt;^&lt;/sup&gt;Xenobiotic resistance (fungicide)&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (fungicide)<sup>^</sup>#gephebase-summary-title</a> )	Trait
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon A
low melanin levels - higher growth rate in absence of fungicide	Trait State in Taxon B

Trait #2	Trait Category
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> )	Category= <sup>^</sup> Physiology <sup>^</sup> #gephebase-summary-title)
Melanin content ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=&lt;sup&gt;^&lt;/sup&gt;Melanin content&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Melanin content<sup>^</sup>#gephebase-summary-title</a> )	Trait
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon A
low melanin levels - higher growth rate in absence of fungicide	Trait State in Taxon B

Data not curated

Ancestral State

Taxonomic Status

Intraspecific (<https://www.gephebase.org/search-criteria?/and+Taxonomic>)

Status=<sup>^</sup>Intraspecific<sup>^</sup>#gephebase-summary-title)

Taxon A	Latin Name	Common Name	Synonyms	Rank	Lineage	Parent	NCBI Taxonomy ID	is Taxon A an Intraspecies?	Taxon A Description
Zymoseptoria tritici	Zymoseptoria tritici	-	Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323	species	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria	Zymoseptoria () - (Rank: genus)	1047171	( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1047171">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1047171</a> )	strain 3D7

Taxon B	Latin Name	Common Name	Synonyms	Rank	Lineage	Parent	NCBI Taxonomy ID	is Taxon B an Intraspecies?	Taxon B Description
Zymoseptoria tritici	Zymoseptoria tritici	-	Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323	species	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria	Zymoseptoria () - (Rank: genus)	1047171	( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1047171">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1047171</a> )	strain 3D1

GENOTYPIC CHANGE

CMR1	Generic Gene Name	Q06F33 ( <a href="http://www.uniprot.org/uniprot/Q06F33">http://www.uniprot.org/uniprot/Q06F33</a> )	UniProtKB Cochliobolus heterostrophus
-	Synonyms	0	GenebankID or UniProtKB
-	String		
-	Sequence Similarities		
	GO - Molecular Function		
	GO:0008270 : zinc ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0008270">https://www.ebi.ac.uk/QuickGO/term/GO:0008270</a> )		
	GO:0003677 : DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003677">https://www.ebi.ac.uk/QuickGO/term/GO:0003677</a> )		
	GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000981">https://www.ebi.ac.uk/QuickGO/term/GO:0000981</a> )		
	GO - Biological Process		
	GO:0006351 : transcription, DNA-templated ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006351">https://www.ebi.ac.uk/QuickGO/term/GO:0006351</a> )		
	GO - Cellular Component		
	GO:0005634 : nucleus ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005634">https://www.ebi.ac.uk/QuickGO/term/GO:0005634</a> )		

Mutation #1

No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title</a> )	Presumptive Null
Cis-regulatory ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title</a> )	Molecular Type
Insertion ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title</a> )	Aberration Type
10-100 kb	Insertion Size
insertion of a transposable element island (13 TE interspersed by simple repeats) of approximately 30 kb, located 1862 bp upstream of Zmr1 start codon - analysis of knock out lines of the TE island insertion	Molecular Details of the Mutation
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title</a> )	Experimental Evidence
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) ( <a href="https://pubmed.ncbi.nlm.nih.gov/30012138">https://pubmed.ncbi.nlm.nih.gov/30012138</a> )	Main Reference
Krishnan P; Meile L; Plissonneau C; Ma X; Hartmann FE; Croll D; McDonald BA; SÃ¡nchez-Vallet A	Authors
Fungal plant pathogens pose major threats to crop yield and sustainable food production if they are highly adapted to their host and the local environment. Variation in gene expression contributes to phenotypic diversity within fungal species and affects adaptation. However, very few cases of adaptive regulatory changes have been reported in fungi and the underlying mechanisms remain largely unexplored. Fungal pathogen genomes are highly plastic and harbor numerous insertions of transposable elements, which can potentially contribute to gene expression regulation. In this work, we elucidated how transposable elements contribute to variation in melanin accumulation, a quantitative trait in fungi that affects survival under stressful conditions.	Abstract
We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen <i>Zysoseptoria tritici</i> . We show that differences in melanin levels between two strains of <i>Z. tritici</i> are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of <i>Z. tritici</i> strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.	
Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.	Additional References

Mutation #2

No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title</a> )	Presumptive Null
Cis-regulatory ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title</a> )	Molecular Type
SNP ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title</a> )	Aberration Type
several candidate SNP - tests using reporter transgenes	Molecular Details of the Mutation
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title</a> )	Experimental Evidence
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) ( <a href="https://pubmed.ncbi.nlm.nih.gov/30012138">https://pubmed.ncbi.nlm.nih.gov/30012138</a> )	Main Reference
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stressful conditions.

We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen *Zymoseptoria tritici*. We show that differences in melanin levels between two strains of *Z. tritici* are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of *Z. tritici* strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.

Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.

[Additional References](#)

## RELATED GEPHE

No matches found.

[Related Genes](#)

No matches found.

[Related Haplotypes](#)

## EXTERNAL LINKS

## COMMENTS

@TE ; check for UniProtKB and orthology with Cmr1